

# SeqServer®

biology in silico

## ClustalW Results

Sequences

Help

Retrieval

BLAST2

FASTA

ClustalW

GCG Assembly

Phrap

Translation

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PF-0066-2DIVSCAH-2  
gi|1363129|pir|D48909

### CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO: 2

Sequence 2: gi|1363129|pir|D48909

161 aa Wilkie et al. GPCR8

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 8

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:744

Alignment Score -27

CLUSTAL-Alignment file created [baa08rUyK.aln]

CLUSTAL W (1.7) multiple sequence alignment

```
PF-0066-2DIVSCAH-2      -----MKAVLLALLMAGLALQPGTALLCYSCKAQVSNED
gi|1363129|pir|D48909  VGVRHSLKYPAIMTERKAAAILALLWAVLVVSVGPLLGWKEPVPPDERF
                        *.:**** * : . .** : . . . .
```

```
PF-0066-2DIVSCAH-2      CLQVENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDSDQYYVGKKN-
gi|1363129|pir|D48909  CGITEEVGYAIFSSVCSFYLPMAVIVVMYCRVYVVARSTTRSLEAGIKRE
                        * .*: . . : .:****: : . . . . * *
```

```
PF-0066-2DIVSCAH-2      -----ITCCDLDLCNX-----SGAHALQPAAAILALLPALGLL
gi|1363129|pir|D48909  PGKASEVVLRIHCRGAATSAKGNPGTQSSKGHTLRSSLSVRLKFSREKK
                        * * .: . * .*: .: : * :
```

```
PF-0066-2DIVSCAH-2      LWGPGQL----
gi|1363129|pir|D48909  AAKTLAIVGV
                        . :
```

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FASTA

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PF-0066-2DIVSCAH-2  
gi|478299|pir||JN0831

### CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO:2

Sequence 2: gi|478299|pir||JN0831

267 aa Wray and Fisher GlnR

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 13

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:747

Alignment Score -2

CLUSTAL-Alignment file created [baa0fhJdp.aln]

CLUSTAL W (1.7) multiple sequence alignment

```
PF-0066-2DIVSCAH-2      -----MKAVLLALLMAGLALQPGTALLCYSCKAQVSNE
gi|478299|pir||JN0831    MSSLLLLTNALQPSTEVLPALGLLHNVVAPAECPALVDTPGADVILVD
                          : *: * * . : * * . * : : :
```

```
PF-0066-2DIVSCAH-2      ---DCLQVENCTQLG---EQCWTARIRAVGLLTVISKGCSLNCVDDSDQ
gi|478299|pir||JN0831    GRRDLPQIRSLCQLLRSTGLSCPLVLIVTEGGLAAVTADWGIDDVLLDTA
                          * * : . . * * . * : * * : : . : : * .
```

```
PF-0066-2DIVSCAH-2      -----YYVGKKNITCCDLDLCNXSGAHALQPAAILALLPALGLL
gi|478299|pir||JN0831    GPAEVEARLRLATGRQQLGGDDSPMEIRNGDLSVDEATYSAKLKGRVLDL
                          . * : : : * : : . * : : : * : * : *
```

```
PF-0066-2DIVSCAH-2      LWGPGQL-----
gi|478299|pir||JN0831    TFKEFELLKYLAQHPRGVFTRAQLLQEVWGYDYFGGTRTVDVHVRRLRAK
                          : : *
```

```
PF-0066-2DIVSCAH-2      -----
gi|478299|pir||JN0831    LGPEHESLIGTVRNVGYRFVTPEKPEKGEKSDKSEKAERA EKAERAETPG
```

PF-0066-2DIVSCAH-2

gi|478299|pir||JN0831

KAAAETNEAAGARSSKV

---

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Help

Retrieval

BLAST2

FASTA



ClustalW

GCG Assembly

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 PF-0066-2DIVSCAH-2  
 gi|730069|sp|Q08326|MSS4\_RAT

### CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

123 aa SEQ ID NO:2

Sequence 2: gi|730069|sp|Q08326|MSS4\_RAT

123 aa Burton ~~et al.~~ MSS4

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 5

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:715

Alignment Score 23

CLUSTAL-Alignment file created [baa0L2OjI.aln]

CLUSTAL W (1.7) multiple sequence alignment

PF-0066-2DIVSCAH-2  
 gi|730069|sp|Q08326|MSS4\_RAT

MKAVLLALLMAGLALQPGTALLCYSCAQVSNECLQVENCTQLGEQCWT  
 MEPCELQNELVSAEGRNRKAVLCQRCGSRV-----LQPGTALFSRRQLFL  
 \*:. \* :.. : .:.\* \* :.\* \*\* .. .\*

PF-0066-2DIVSCAH-2  
 gi|730069|sp|Q08326|MSS4\_RAT

ARIRAVGLLTVIS--KGC SLNCVDDSDYVVGK-----KNITCC  
 PSMRKKPDLVDGSDPDGVLEEHVLVNDMFIFENVGFTKDVGNVFLVCA  
 .:\* .\*. \* .\* \*: :\* : : \*

PF-0066-2DIVSCAH-2  
 gi|730069|sp|Q08326|MSS4\_RAT

DTDLCNXSGAHALQAAAILALLPALGLLLWGPGQL  
 DCEIGP-IGWHCLDDKNSFYVALERSHE-----  
 \* : : \* \*. \* : : . \* : .

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[Sequences](#)[Help](#)[Retrieval](#)[BLAST2](#)[FASTA](#)[ClustalW](#)[GCG Assembly](#)[Phrap](#)[Translation](#)

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 PF-0066-2DIVSCAH-2  
gi|530797|gb|AAA20877.1|

### CLUSTAL W (1.7) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: PF-0066-2DIVSCAH-2

Sequence 2: gi|530797|gb|AAA20877.1|

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 13

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Delayed

Sequence:1 Score:0

Sequence:2 Score:538

Alignment Score 12

CLUSTAL-Alignment file created [baa9Wed\_\_.aln]

CLUSTAL W (1.7) multiple sequence alignment

123 aa SEQ ID NO:2  
88 aa Birkeland ~~del~~. LysA

PF-0066-2DIVSCAH-2  
gi|530797|gb|AAA20877.1|

MKAVLLALLMAG----LALQPGTALLCYSCAQVSNECLQVENCTQLGE  
MNQINWKLRLKSKAFWLALLPALFLLIQAIGASFG-----YKWNFVILNQ  
\*: : \* : . \*\*\* \* . \*\* : \*... \* . \*:

PF-0066-2DIVSCAH-2  
gi|530797|gb|AAA20877.1|

QCWTARIRAVGLLTVISKGCSLNCVDDSDYVVGKN-ITCCDTLDCNXS  
QLAAVVNAAFALLAIV--G----VVADPTTSGLGDSDRVLNKDKSEENK-  
\* :. \*...\*: : \* \* . :\*... : \*... \*

PF-0066-2DIVSCAH-2  
gi|530797|gb|AAA20877.1|

GAHALQPAAAILALLPALGLLLWGPGQL  
-----

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<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>